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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Wed Aug 20 09:44:12 1997; MasPar time 12:79 Seconds 665.067 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-469-637A-2 (1-401) from US08469637A.pep (1 of 2) 3030

1 MNKLLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: PAM 150 Gap 11

Searched: 59021 segs, 21210388 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 48.313; Variance 81.174; scale 0.595

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22	20	19	18	17	16	15	14	13	12	H	10	9	ထ	7	o,	S	4	ω	N	₩.	ult No.
146 144	159	159	172	178	186	188	207	213	215	220	221	233	260	260	265	269	294	303	375	405	Score
																		0	N	13.4	Query Match
271	260	256	455	595	461	323	425	427	416	461	454	349	435	325	415	326	289	277	474	461	Length
7 '	1 10	_	9	N	φ	w	σ	σ	σ	9	9	10	9	10	φ	10	N	2	9	9	BG
OX40_MOUSE	CD27_HUMAN	41BB_MOUSE	TNR1_HUMAN	CD30_HUMAN	TNR1_PIG	FASA_BOVIN	NGFR_RAT	NGFR_HUMAN	NGFR_CHICK	TNR1_RAT	TNR1_MOUSE	VC22_VARV	TNRC_HUMAN	VT2_SFVKA	TNRC_MOUSE	VT2_MYXVL	CD40_MOUSE	CD40_HUMAN	TNR2_MOUSE	TNR2_HUMAN	ID
RECEPTOR	RECEPTOR	LIGAND RE	TUMOR NECROSIS FACTOR	CD30L RECEPTOR PRECUR	TUMOR NECROSIS FACTOR	FASL RECEPTOR PRECURS	LOW-AFFINITY NERVE GR				SIS	PROTEIN C22/B28 HOMOL	LYMPHOTOXIN-BETA RECE	TUMOR NECROSIS FACTOR	LYMPHOTOXIN-BETA RECE	TUMOR NECROSIS FACTOR	CD40L RECEPTOR PRECUR	CD40L RECEPTOR PRECUR	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	Description
. 73	44.	٠.	1.29e-13	.30e-	.66e-	.08e-	.87e-2	.15e-2	3e-2	.35e-2	.72e-2	.20e-2	.97e-3	.97e-	.70e-	.38e-3	.50e-3	.03e-	.05e-	w	Pred. No.
	146 4.8 2/1 / OX40_KAT OX40L RECEPTOR PRECUR 1.70	159 5.2 260 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.4 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.6 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.7	159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.4 159 5.2 260 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.4 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.6 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.7	172 5.7 455 9 TURL HUMAN TUMOR NECROSIS FACTOR 1.2 159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.4 159 5.2 260 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.4 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.6 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.7	178 5.9 5.9 5.0 CD30_HUMAN CD30L RECEPTOR PRECUR 9.30e- 172 5.7 455 9 TIRR_HUMAN TUMOR NECROSIS FACTOR 1.29e- 159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e- 159 5.2 260 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.45e- 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e- 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-	186 6.1 461 9 TUNAL PIG TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 5.9 CD30_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 172 5.7 455 9 TURL HUMAN TUMOR NECROSIS FACTOR 1.29e-1 159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 159 5.2 256 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.45e-1 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 146 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	188 6.2 323 \$ FASA_BOVIN FASL RECEPTOR PRECURS 1.08e-1 186 6.1 461 9 TURI_PIC TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 5.9 2 CD30_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 172 5.7 455 9 TURI_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 159 5.2 256 1 41BB_MOUSE 4-1BB_LIGAND RECEPTOR 3.45e-1 159 5.2 260 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.45e-1 146 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	207 6.8 425 6 NGFR_RAT LOW AFFINITY NERVE GR 1.87e-2 188 6.2 33 FASA_BOVIN FASL RECEPTOR PRECURS 1.08e-1 186 6.1 461 9 TURL_PIG TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 595 2 CD30_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 179 5.7 455 9 TURL_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 159 5.2 256 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.45e-1 144 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	213 7.0 427 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 207 6.8 425 6 NGFR_HAT LOW-AFFINITY NERVE GR 1.17e-2 188 6.2 323 FASA_BOVIN FASL RECEPTOR PRECURS 1.08e-1 186 6.1 461 9 TNR1_PIG TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 595 2 CD30_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 179 5.7 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 159 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 159 5.2 256 2 CD27_HUMAN CD47L RECEPTOR PRECUR 7.67e-0 146 4.8 271 7 OX40_MOUSE OX40L RECEPTOR PRECUR 7.67e-0 147 148 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	215 7.1 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 4.53e-2 213 7.0 427 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.18c-2 207 6.8 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.8fe-2 207 6.8 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.8fe-2 208 6.2 323 FASA_BOVIN FASL RECEPTOR PRECURS 1.08e-1 209 186 6.1 461 9 TNR1_PIG TUMOR NECROSIS FACTOR 2.66e-1 200 186 6.1 461 9 TNR1_PIG TUMOR NECROSIS FACTOR 2.66e-1 201 186 6.1 461 9 TNR1_PIG TUMOR NECROSIS FACTOR 2.66e-1 201 197 201 197 201 197 201 201 201 201 201 201 201 201 201 201	220 7.3 461 9 TURL_RAT TUMOR NECROSIS FACTOR 4.35e-2 215 7.1 416 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 213 7.0 427 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 207 6.8 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.87e-2 208 6.2 323 3FASA_BOVIN FASL_RECEPTOR PRECURS 1.08e-1 186 6.1 461 9 TURL_PIG TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 5.7 45.9 TURL_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 179 5.7 45.9 TURL_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 189 5.2 256 1 41BB_MOUSE 4-1BB_LIGAND RECEPTOR 3.45e-1 189 5.2 256 2 CD27_HUMAN CD27L RECEPTOR PRECUR 3.45e-1 140 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 141 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	221 7.3 454 9 TNR1_MOUSE TUMOR NECROSIS FACTOR 2.72e- 220 7.3 461 9 TNR1_RAT TUMOR NECROSIS FACTOR 4.35e-2 215 7.1 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 4.53e-2 217 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 1.15e-2 218 6.2 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.15e-2 219 6.2 323 FASA_BOVIN FASL RECEPTOR FRECURS 1.08e-1 218 6.1 461 9 TNR1_PIG CUMOR NECROSIS FACTOR 2.66e-1 217 25.7 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 215 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 216 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 217 0X40_MOUSE OX40L RECEPTOR PRECUR 7.67e-0 218 0X40_MOUSE OX40L RECEPTOR PRECUR 1.73e-0	233 7.7 349 10 VC22_VARV PROTEIN C22/B28 HOMOL 9.20e-2 221 7.3 461 9 TURI_MOUSE TUMOR NECROSIS FACTOR 2.72e-2 220 7.3 461 9 TURI_RAT TUMOR NECROSIS FACTOR 4.35e-2 215 7.1 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 4.53e-2 216 7.0 427 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.87e-2 207 6.8 42.5 6 NGFR_HOMAN LOW-AFFINITY NERVE GR 1.87e-2 188 6.2 32.3 FASA_BOVIN FASL RECEPTOR FRECURS 1.08e-1 186 6.1 461 9 TURI_FIG TUMOR NECROSIS FACTOR 2.66e-1 178 5.9 595 2 CD30_HUMAN CD30L RECEPTOR FRECUR 9.30e-1 179 5.7 455 9 TURI_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 179 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 164 4.8 271 7 OX40_MOUSE OX40L RECEPTOR FRECUR 7.67e-0 179-0	260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN-BETA RECE 1.97e-3 233 7.7 454 9 TURL_MOUSE TUMOR NECROSIS FACTOR 2.72e-2 221 7.3 451 9 TURL_RAT TUMOR NECROSIS FACTOR 4.35e-2 220 7.3 461 9 TURL_RAT TUMOR NECROSIS FACTOR 4.35e-2 231 7.0 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 1.15e-2 207 6.8 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.15e-2 207 6.8 425 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.87e-2 218 6.2 323 FASA_BOVIN FASL RECEPTOR PRECURS 1.08e-1 219 5.9 5.7 455 9 TURL_HUMAN CD30L RECEPTOR PRECUR 9.30e-1 25.7 455 9 TURL_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 260 2 CD30_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 27.7 45.9 TURL_HUMAN TUMOR NECROSIS FACTOR 3.45e-1 28.7 45.9 TURL_HUMAN CD30L RECEPTOR PRECUR 3.45e-1 29 5.2 256 1 41BB_MOUSE 4-1BB_LIGAND RECEPTOR PRECUR 7.67e-0 20 7.40_MOUSE 0X40L RECEPTOR PRECUR 7.67e-0 20 7.40_MOUSE 0X40L RECEPTOR PRECUR 1.73e-0	260 8.6 33.5 10 VT2_SFYKA TUMOR NECROSIS FACTOR 1.97e-3 260 8.6 43.5 9 VRC_HUMAN LYMPHOTOXIN-BETA RECE 1.97e-3 270 7.3 34.9 10 VC22_VARV PROTEIN C22_D28 HOMOL 9.20e-2 271 7.3 45.4 9 TINRL_MOUSE TUMOR NECROSIS FACTOR 2.72e-2 272 7.3 45.4 9 TINRL_MOUSE TUMOR NECROSIS FACTOR 4.55e-2 273 7.0 41.6 6 NGFR_CHICK LOW-AFFINITY NERVE GR 4.53e-2 274 41.6 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 275 7.1 41.6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 276 8.2 32 FASA_BOVIN FASL RECEPTOR FRECURS 1.08e-1 277 8.5 9 TINRL_MUMAN TUMOR NECROSIS FACTOR 2.66e-1 278 1.5 9 5030_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 279 5.2 256 1 41BB_MOUSE 4-1BB LIGAND RECEPTOR 3.45e-1 270 7 0X40_RAT 0X40L RECEPTOR PRECUR 7.67e-0 278 1.79e-0 278	265 8.7 415 9 TURC_MOUSE LYMPHOTOXIN BETA RECE 1.70e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 273 7.7 449 9 TURL_MOUSE TUMOR NECROSIS FACTOR 2.72e-2 273 461 9 TURL_MAT TUMOR NECROSIS FACTOR 4.35e-2 273 461 9 TURL_RAT TUMOR NECROSIS FACTOR 4.53e-2 275 7.1 416 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 276 8.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 277 425 9 TURL_HUMAN LOW-AFFINITY NERVE GR 1.15e-2 278 425 9 TURL_HUMAN TUMOR NECROSIS FACTOR 2.66e-1 279 5.7 455 9 TURL_HUMAN TUMOR NECROSIS FACTOR 2.66e-1 270 425 1 141B_MOUSE TUMOR NECROSIS FACTOR 1.29e-1 270 4.8 271 7 OX40_RAT OX40L RECEPTOR PRECUR 3.45e-1 271 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 272 1 173e-0	269 8.9 325 10 VT2_WYXVL TUMOR NECROSIS FACTOR 2.38e-3 260 8.6 325 10 VT2_SFVKA TUMOR NECROSIS FACTOR 1.97e-3 260 8.6 435 9 TNRC_HUMAN LYMPHOTOXIN-BETA RECE 1.97e-3 260 8.6 435 9 TNRC_HUMAN LYMPHOTOXIN-BETA RECE 1.97e-3 260 8.6 435 9 TNRC_HUMAN LYMPHOTOXIN-BETA RECE 1.97e-3 270 349 10 VC22_VARV PROTEIN C227_B28 HOMOL 9.20e-2 221 7.3 461 9 TNR1_RAIT TUMOR NECROSIS FACTOR 4.35e-2 271 7.0 426 6 NGFR_CHICK LOW-AFFINITY NERVE GR 1.5e-2 271 7.0 427 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.87e-2 271 7.0 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.87e-2 271 7.0 425 6 NGFR_HOWAN LOW-AFFINITY NERVE GR 1.87e-2 272 7.0 425 9 TNR1_PIG TUMOR NECROSIS FACTOR 2.66e-1 273 7.1 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 3.6e-1 274 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 3.6e-1 275 276 1418B_MOUSE 4-188 LIGAND RECEPTOR BRECUR 3.45e-1 276 4.8 271 7 OX40_MOUSE OX40L RECEPTOR PRECUR 7.67e-0 277 144 4.8 272 7 OX40_MOUSE OX40L RECEPTOR PRECUR 7.67e-0	294 9.7 289 2 CD40_MOUSE CD40L_RECEPTOR_PRECUR_9.50e-3 269 8.7 415 9 TWRC_MOUSE LYMPHOTOXIN_BETA_RECE_1.70e-3 260 8.6 435 9 TWRC_HOWAN RECROSIS_FACTOR_1.97e-3 260 8.6 435 9 TWRC_HOWAN LYMPHOTOXIN_BETA_RECE_1.70e-3 260 8.6 435 9 TWRC_HOWAN LYMPHOTOXIN_BETA_RECE_1.97e-3 260 8.6 435 9 TWRC_HOWAN LYMPHOTOXIN_BETA_RECE_1.97e-3 270 7.3 454 9 TWRL_MOUSE TUMOR_NECROSIS_FACTOR_2.72e-2 271 7.3 454 9 TWRL_RAT TUMOR_NECROSIS_FACTOR_2.72e-2 272 7.1 416 6 NGFR_CHICK_COW-AFFINITY_NERVE_GR_1.15e-2 273 7.0 427 6 NGFR_HOWAN LOW-AFFINITY_NERVE_GR_1.15e-2 270 6.1 451 9 TWRL_RAT LOW-AFFINITY_NERVE_GR_1.15e-2 270 7.6 461 9 TWRL_PIG_TUMOR_NECROSIS_FACTOR_2.66e-1 271 7.3 454 9 TWRL_PIG_CD30L_RECEPTOR_PRECUR_3.45e-1 272 7.4 455 9 TWRL_HOWAN TUMOR_NECROSIS_FACTOR_1.29e-1 273 7.5 455 9 TWRL_HOWAN TUMOR_NECROSIS_FACTOR_1.29e-1 274 4.8 272 7 OX40_MOUSE_OX40L_RECEPTOR_PRECUR_3.45e-1 275 7.7 4.8 272 7 OX40_MOUSE_OX40L_RECEPTOR_PRECUR_1.73e-0	303 10.0 277 2 CD40_HUMAN CD401_RECEPTOR PRECUR 1.03e-4 294 9.7 289 2 CD40_MOUSE CD401_RECEPTOR PRECUR 1.03e-4 265 8.7 415 9 TURC_MOUSE LYMPHOTOXIN BETA RECE 1.70e-3 266 8.6 435 9 TURC_MOUSE TUMOR NECROSIS FACTOR 1.97e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 261 8.6 435 9 TURC_HUMAN LYMPHOTOXIN BETA RECE 1.97e-3 262 7.3 454 9 TURL_RAT TUMOR NECROSIS FACTOR 2.72e-7 273 7.1 416 6 NGFR_CHICK LOW-AFFINITY NERVE GR 4.53e-7 274 455 9 TURL_RAT LOW-AFFINITY NERVE GR 1.15e-7 275 7.1 416 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 276 8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 277 458 9 TURL_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 278 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 279 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 280 7.1 416 9 TURL_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 290 7.3 461 9 TURL_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 201 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.15e-7 202 7.4 55 9 TURL_HUMAN TUMOR NECROSIS FACTOR 2.66e-1 203 7.4 425 9 TURL_HUMAN TUMOR NECROSIS FACTOR 2.66e-1 204 7.5 455 9 TURL_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 205 7.4 425 0 TURL_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 207 6.8 425 0 TURL_HUMAN TUMOR NECROSIS FACTOR 3.45e-1 208 7.6 425 0 TURL_HUMAN CD27_RECEPTOR PRECUR 7.67e-0 209 7.6 426 0 TURL_HUMAN CD27_RECEPTOR PRECUR 7.67e-0 200 7.6 426 0 TURL_HUMAN CD27_RECEPTOR PRECUR 1.73e-0	375 12.4 474 9 TUR2_MOUSE TUMOR NECROSIS FACTOR 9.05e-5 303 10.0 277 2 CD40_MOUSE CD40L RECEPTOR PRECUR 1.03e-4 294 9.7 289 2 CD40_MOUSE CD40L RECEPTOR PRECUR 9.50e-3 269 8.9 326 10 VT2_MYXVL TUMOR NECROSIS FACTOR 2.38e-3 260 8.6 325 10 VT2_SYVKA TUMOR NECROSIS FACTOR 1.70e-3 260 8.6 435 9 TURC_MOUSE TUMOR NECROSIS FACTOR 1.97e-3 260 8.6 435 9 TURC_HUMAN LYMPHOTOXIN_BETA RECE 1.70e-3 273 7.7 3454 9 TURL_MOUSE TUMOR NECROSIS FACTOR 2.20e-2 221 7.3 461 9 TURL_RAT TUMOR NECROSIS FACTOR 4.35e-2 271 7.3 461 9 TURL_RAT TUMOR NECROSIS FACTOR 4.35e-2 271 7.0 426 6 NGFR_CHICK LOW-AFFINITY NERVE GR 1.87e-2 273 6.8 4.25 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.87e-2 274 6.8 4.25 6 NGFR_RAT LOW-AFFINITY NERVE GR 1.87e-2 275 7.0 426 6 NGFR_BAT LOW-AFFINITY NERVE GR 1.87e-2 276 6.8 4.59 9 TURL_PIG TUMOR NECROSIS FACTOR 2.66e-1 277 4.55 9 TURL_HUMAN TUMOR NECROSIS FACTOR 2.66e-1 278 5.2 2.56 1 418B_MOUSE 4-18B_LGAND RECEPTOR PRECUR 3.45e-1 279 5.2 2.56 1 418B_MOUSE 5.27 RECEPTOR PRECUR 3.45e-1 270 7 OX40_RAT OX40L RECEPTOR PRECUR 7.67e-0 271 1.73e-0	3.4 461 9 TNR2_HUMAN TUMOR NECROSIS FACTOR 1.38e-6 2.4 474 9 TNR2_MOUSE TUMOR NECROSIS FACTOR 9.05e-5 0.0 277 2 CD40_HUMAN CD40L RECEPTOR PRECUR 1.03e-4 9.7 289 2 CD40_MOUSE CD40L RECEPTOR PRECUR 9.50e-3 8.9 326 10 VT2_MYXVL TUMOR NECROSIS FACTOR 2.38e-3 8.6 325 10 VT2_SFVKA TUMOR NECROSIS FACTOR 1.97e-3 8.6 325 10 VT2_SFVKA TUMOR NECROSIS FACTOR 1.97e-3 8.6 325 10 VT2_SFVKA TUMOR NECROSIS FACTOR 1.97e-3 8.6 325 10 VT2_SFVKA TUMOR NECROSIS FACTOR 2.72e-2 7.3 454 9 TNR1_MOUSE TUMOR NECROSIS FACTOR 2.72e-2 7.3 454 9 TNR1_RAT TUMOR NECROSIS FACTOR 2.72e-2 7.3 461 9 TNR1_RAT TUMOR NECROSIS FACTOR 2.72e-2 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.5e-2 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.5e-2 6.8 425 6 NGFR_HUMAN LOW-AFFINITY NERVE GR 1.5e-2 6.9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.08e-1 1.5 9 TNR1_HUMAN TUMOR NECEPTOR PRECURS 9.30e-1 9.7 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 9.7 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 9.7 455 9 TNR1_HUMAN TUMOR NECROSIS FACTOR 1.29e-1 9.7 456 1 41BB MOUSE 4.1BB LIGAND RECEPTOR 9.30e-1 9.7 456 1 41BB MOUSE 4.1BB LIGAND RECEPTOR 3.45e-1 9.7 0X40_MOUSE 4.1BB LIGAND RECEPTOR 7.67e-0 9.7 0X40_MOUSE 0.740L RECEPTOR PRECUR 7.67e-0

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97	96	98	96	96	96	98	96	99	100	101	101	102	105	110	115	124	124	134	134	137	140	141
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		MYSC		XCPE														FASA	CD27	FASA	1 41BB_HUMAN	7 OX40_HUMAN
DYNEIN HEAVY CHAIN, C	BASEMENT MEMBRANE-SPE	MYOSIN HEAVY CHAIN C	PROBABLE SERINE/THREO	CHROMOSOME ASSEMBLY P	VALYL-TRNA SYNTHETASE	PRE-MRNA SPLICING FAC	PHOSPHATE REGULON SEN	PUTATIVE TRANSLATIONA	DESMOPLAKIN I AND II	HYPOTHETICAL 128.8 KD	GLUCOSAMINE FRUCTOSE	LAMININ ALPHA-1 CHAIN	VON WILLEBRAND FACTOR	CAMP-REGULATED D2 PRO	HYPOTHETICAL 41.6 KD		PROTEIN A53.	FASL RECEPTOR PRECURS	CD27L RECEPTOR PRECUR		4-1BB LIGAND RECEPTOR	OX40L RECEPTOR PRECUR
38e-	38e	91e	38e	38e	7.38e-01	91e	38e	84e	2.05e-01	486	1.48e-01	06e	90e	01e	19∈	5	4.35e-05	5	9.35e-07	7e-	8.68e-08	5.81e-08

ALIGNMENTS

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CHÂRACTERIZATION. MEDLINE; 93016040. PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M., LIPARI M.T., GOEDDEL D.V.;	SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362. MEDLINE; 91056048. LOETSCHER H., SCHLAEGER E.J., LAHM HW., PAN YC.E., LESSLAUER W., EROCKHAUS M.; J. BIOL. CHEM. 265:20131-20138(1990). [6]	.M.; L. ACAD. SCI. U.S.A. 87:6151-6155(1990). OF 27-31. 90110215. H., NOVICK D., WALLACH D.; CHEM. 265:1531-1536(1990).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 91045991. KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W., HALE K.K., SQUIRES G.H., THOMPSON R.C., VANNICE J.L.; PROG. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990). [3] [3] SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE; 90349572. HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,	HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. [1] SEQUENCE FROM N.A. MEDLINE; 90260639. SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R., SCIENCE 248:1019-1023(1990).	TYR2_HMAN STANDARD; PRT; 461 AA. P20333; P20333; P1-FEB-1991 (REL. 17, CREATED) O1-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE) O1-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B). TNFR2 OR TNEBR.

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TINR2_MOUSE STANDARD P25119;
01-MAY-1992 (REL. 22, C 01-MAY-1992 (REL. 22, L 01-OCT-1996 (REL. 34, L TUMOR NECROSIS FACTOR R TNER2 OR TNER-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
REPEAT
RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. BIOL. CHEM. 267:21172-21178(1992).

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

-!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

EMBL: M33315; G189186; -.

EMBL: M33315; G189186; -.

EMBL: M35857; G339752; -.

EMBL: M35857; G339758; -.

PIR: A35607; A36007.

PIR: A35607; A36075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION
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   MUSCULUS
                                                                                                                                                                                                                                                                                                                             CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS
                                                                                                                                                                                               OYVKOECNRTHNRVCECKEGRY -- LEI - EFC - L - KH - RSCPPGFGVVQAGTPERNTVCKR
                                                                                                                                                                                                                                                                YDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A23666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P19438; 1TNR
                                                                                                                                                                                                                                                                                                                                                                         13.48;
Similarity 41.88;
69; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                             161 AA;
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   (MOUSE)
                                                                                                               STANDARD;
                                               22, CREATED)
22, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48316 MW;
                                 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN; REPEAT; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                           Score 405; DB 9;
Pred. No. 1.33e-63;
26; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

R -> P (IN

R -> M (IN

A -> T (IN
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THER-CYS 4.
BY SIMILARI
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TNFR-CYS 1.
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-> M (IN
-> T (IN
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                                PRECURSOR (INF-R2) (P75).
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N REF. 1).
N REF. 3).
CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 461;
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                                                                                                                                                                                189
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Best Loc
Matches
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MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A
WONG G.H., CHEN E.Y., G
                                             CD40_HUMAN STANDARD; PRT; 277 AA. P25942; P15942; CREATED) 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. CELL. BIOL. 11:3020 JOHN CL. CELL. BIOL. 11:3020 JOHN CL. CELL. BIOL. 11:3020 JOHN C. CELL. BIOL. 11:3020 JOHN C. FUNCTION: RECEPTOR FOR TWE-BRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-****TUARITY: CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
EUTHERIA; R
                CD40L RECEPTOR CD40.
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REPEAT
REPEAT
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DOMAIN
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CHAIN
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HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOODWIN R.G., ANDERSON COPELAND N.G., JENKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 91246168.
                                                                                                                                                                                151
                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                             86
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                                                                                                                                                                         tkqqnrvcaceagrycalkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtf 171
                                                                                                                                                                                                                                                                                                                           OLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQEC 97
                                                                                                                                                                                                                                           NRTHNRVCECKEGRY - - LEIEF - - CLKH - R - S - CPPGFGVVQAGTPERNTVCKRCPDGFF
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
66; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAD.
                                                                                                                                                                                                                                                                                                                                                                         12.4%;
larity 41.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DERSON D., JERZY R.,
ENKINS N.A., SMITH C.
11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI.
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GOEDDEL D.V.;
. U.S.A. 88:2830-2834(1991).
                              (B-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN; REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           MW,
                                                                                                                                                                                                                                                                                                                                                                         Score 375; DB 9;
Pred. No. 9.05e-57;
21; Mismatches 61
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POTENTIAL.
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CYTOPLASMIC (E
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                                SURFACE ANTIGEN CD40) (BP50) (CDW40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                           206
                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                       Length 474;
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Best Local Similarity
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EUTHERIA; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (REL. 23, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
           SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 93094586.
GRIMALDI J.C., TORRES R., KO
                                                                                                                                                                                  STRAIN-BALB/C;
TORRES R.M.;
                                                                                                                                                                                                                                                                                                   MEDLINE; 92105763.
TORRES R.M., CLARK E.A.;
J. IMMUNOL. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
FITKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAMENKOVIC I., CLARK E.A., EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 89356608.
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IM; 109535; -.
                                                                                                                                                       UBMITTED (SEP-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS
:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
:- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCING
:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tsetdtictceegwhctseacescvlhrscspgfgvkqiatgvsdticepcpvgffsnvs 155
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GLYCOPROTEIN;
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                                                                                                                                                             EMBL/GENBANK/DDBJ DATA BANKS
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                 KOZAK C.
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21; Mismatches
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Pred. No. 1.03e-40;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
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Best Local
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01-APR-1993
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                                         PROSITE; F
RECEPTOR;
SIGNAL
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SEQUENCE
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DOMAIN
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EMBL; M94126; G192526;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 91335768.
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Similarity 38.8%;
59; Conservat
E195.
; GCYZML.
38; ITNR.
38; ITNR.
PS00652; TNFR_NGFR.
A; GLYCOPROTEIN; REPF
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186
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3 (REL. 25,
4 (REL. 28,
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EMBL; M94128; G192526; JOINED.
EMBL; M94128; G192526; JOINED.
EMBL; M94127; G192526; JOINED.
PIR; A46476; A46476.
HSSP: P10479.
                                                                                                                  UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
VIROLOGY 184:370-382(1991).

- FUNCTION: BINDS TO THE ALPHA AND BETA. PROBABLY PREVENTS THE TREACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-- INTIVIRAL EFFECTS OF THE CYTOKINE.

-- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; M95181; G332310; -.
EMBL; A23729; E199442; -.
FIR; A40566; GQVML.
HSSP; P19438; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYXOMA VIRUS (STRAIN LAUSANNE).
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR; B-CELL; GLYCOPROTEIN;
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:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                        REPEAT; SIGNAL
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Pred. No. 9.50e-39;
20; Mismatches 65;
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CYTOPLASMIC (POTENTIAL).
4 x THER-CYS.
TIMER-CYS 1.
TIMER-CYS 2.
TIMER-CYS 3.
TIMER-CYS 4.
POTENTIAL.
PROTEIN T2.
4 X TNFR-CYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               POXVIRIDAE; CHORDOPOXVIRINAE;
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EMBL; L38423; G600223;
EMBL; U30798; G1061327
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REPEAT
                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                            NAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T.,
                                                                                                                                                                                                                                                                                                                 STRAIN-CVB; TISSUE-LUNG;
FORCE W.R., WILLIAMS-ABBOTT L.,
WARE C.F.;
                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                  REPEAT
                                                              REPEAT
                                                                        REPEAT
                                                                                                                                                                                                                                           GENOMICS 30:312-319(1995)
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 96163885.
                                                                                                                                                                                                                                                                                                       SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INRC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 8.9%;
Local Similarity 33.8%;
ses 47; Conservative
                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                      IMMUNE DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKAPCRKHINC-SV-FGL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sstetctssfnyisvefnl 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNRVCECKEGRY -- LE-IEFC-L-KHRS-CPPGFGVVQAGTPERNTVCKRCPDGFFSNET 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rdrvcdcsagnycllkgqegcricapktkcpagygvs-ghtrtgdvlctkcprytysdav 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctscppgsyasrlcgpgsdtvcspcknetftastnhapacvscrgrctghlsesgscdkt 99
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63
105
148
148
181
205
238
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05 147
186
186
181
205
238
35208 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                        GLYCOPROTEIN; REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
25; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 269; DB 10;
Pred. No. 2.38e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
TNFR-CYS 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                CYTOPLASMIC (POTENTIAL)
4 X TNFR-CYS.
TNFR-CYS 1.
                                                              TNFR-CYS 3
                                                                                                                POTENTIAL.
                                                                                                                          LYMPHOTOXIN-BETA
EXTRACELLULAR (PO
                                                                                                                                             POTENTIAL
                                                                        INFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2F059A61 CRC32;
                                                                                                                                                                                                                                                                                                                          BROWNING J., HESSION C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 AA
                                                                                                                                                                                                                                                                                                       DATA BANKS
                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                              SASAYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
                                                                                                                                                                                                                               POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                           TIZARD
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Best Local S
Matches 5
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P25943;
O1-MAY-1992 (REL. 22, CREATED)
O1-MAY-1992 (REL. 22, LAST SEQUI
O1-FEB-1994 (REL. 28, LAST ANNO
TUMOR NECROSIS FACTOR SOLUBLE RI
        CHAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
CARBOHYD
CARBOHYD
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                  SIGNAL
                                                                                                                                         EMBL; M17433; -; NOT_ANNOTATED_CDS
EMBL; A23727; E199408; -.
PIR; B43692; B43692.
                                                                                                                                                                     BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).
-!- FUNCTION: BINDS TO THE FALPHA AND BETA. PROBABLY PREVENTS THE POTENTIAL REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                               MEDLINE: 91207415.
SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., MCFADDEN G., GOODMIN R.G.;
MCFADDEN G., GOODMIN 776:335-342(1991).
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 87321103.
UPTON C., DELANGE A.M., M
VIROLOGY 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                      SHOPE FIBROMA VIRUS VIRIDAE; DS-DNA ENVI
                                                                                                                      HSSP; P19438; 1
PROSITE; PS0065
                                                                                                                                                                                                                                                       FUNCTION.
                                                                                                                                                                                                                                                                                                                             EPORIPOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VK-QECNTHNRÖCECKEGR---YLEIE--FCLKHR-S-CPPGFGV-VQAGTPERNTVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eevapctsdrkaecrcqpgmscvyldnecvhceeerlvlcqpgteaevtdeimdtdvncv 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE-LQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 8.7%;
Similarity 28.9%;
54; Conservative
                                                                                                             GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
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126
139
142
172
                                                                                                                               LINR.
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                                                                                                                                                                                                                                                                                                                                     IRUS (STRAIN KASZA)
ENVELOPED VIRUSES;
                                                                                                                       TNFR_NGFR
16
325
186
162
104
1186
1186
1205
1205
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132
150
169
187
187
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                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
SOLUBLE RECEPTOR PREC
                                                                                                           REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                     MCFADDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 265; DB 9;
Pred. No. 1.70e-32;
30; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                          PROTENTIAL.
PROTEIN 12.
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
; 3C5DD121 CRC32;
                                                                                                                                                                                                                                                                                                                                      (SFV).
POXVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                      325
                                                                                                                                                                                                                                                                                                                                                                    UPDATE)
R PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                      ያ
                                                                                                                                                                                                                                                                                                                                       CHORDOPOXVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 415;
                                                                                                                                                                                                                                                                                                                                                                    (PROTEIN T2).
                                                                                                                                                                                                                                   NOLAN
                                                                                                                                                                                                                                  0
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CARBOHYL

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Best Local
Matches
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DISULFID DISULFID
                                                                                                                               REPEAT
REPEAT
                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                   CROWE P.D., VAN ARSDALE T.L., WALTER B.N., WARE CEHRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R. SCIENCE 264:707-710(1994).

-i- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
11-YMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNRC_HUMAN STA
P36941;
01-JUN-1994 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 93252381.
BAENS M., CHAFFANET M., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFCR.
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                              HSSP;

    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICHEMBL; L04270; G339762; -.

                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94225209
                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSUE-LIVER;
                                                                                                                                                                                                                                                                                         600979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sptercgtsfnyisvgfnlypvnetscttt-aghneviktkeftvtl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNRVCECKEGRY--L--EIE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hdrvcncstgnycllkgqngcricapqtkcpagygvs-ghtragdtlcekcpphtysdsl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDKCPPGTYLKOHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
                                                                                                                                                                                                                                                                  P19999; 1CLG.
TE; PS00652; TNFR_NGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 8.6%;
Similarity 30.5%;
51; Conservative
325
                                                                                                                                                                                                                                                                                                                                                                       VAN ARSDALE T.L., WALTER B.N., WARE C.F., BROWNING J.L., DIN W.S., GOODWIN R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35132
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CASSIMAN
                                                                                                                                                                                                                                          GLYCOPROTEIN; REPEAT; SIGNAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 260;
Pred. No. 1.
31; Mismatc
BY SIMILARITY.
                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                 TNFR-CYS 3.
                                                                                                                                                                                                                 LYMPHOTOXIN-BETA EXTRACELLULAR (PO
                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C9D2C87B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           re 260; DB 10; d. No. 1.97e-31; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                    POSSIBLE FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                           , HESSION
SMITH C.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
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                                                                                                                                                                                                                                                                            CC -:- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
DR EMBL; X69198; 6457087; -.
PR EMBL; X67117; G516449; -.
R PIR; D30858; D36858.
PIR; S35987; S35987.
PIR; S46888; S46888.
HSSP; P19438; 17NP
PROSTTE
RESULT
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                                                                                                          밁
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Best Local Similarity 32.3%;
Matches 52; Conservative
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 54; Conser
TNR1_MOUSE
P25118;
01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIOLA VIRUS.
VIRIDAE; DS-DNA
ORTHOPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VC22_VARV
                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P34015;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN C22/B28 HOMOLOG
                                                                                                                                                                                                                                                                                                                            REPEAT.
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                                                                                                                                  58
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|: :| ::| | | : | : | : |
                                                                                                                                              ssgckacvsqtkcgigygvs-ghtsvgdvicspcgfgtyshtvssadkc
                                                                                                                                  WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ckaghfqntsspsarcqphtrcengglveaapgtaqsdttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYVKQECNRTHNRVCECKEGRY-----LEIEFCLKHRSCPPGFGV-VQAGTPERNTVCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eeiap-ctskrktgcrcqpgmfcaawalecthcellsdcppgteaelkdevgkgnnhcvp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETSHOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL 90
                                                                                  -IE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPC
                                                                                                                                                                               MNKLLCCALVFLD-ISIKWTTQETFPPKYLHYDE-E-TSHQLLCDKCPPGTYLKQHCTAK
                                                                                                                                                                                                                                                                            31
31
67
349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
435 AA;
(REL.
                                                                                                                                                                                                                              Conservative
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENVELOPED VIRUSES;
22,
                                                                                                                                                                                                                                                                             108
66
108
38189
                                                                                                                                                                                                                                          7.78;
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 CREATED)
LAST SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 260; DB 9;
Pred. No. 1.97e-31;
23; Mismatches 75
                                                                                                                                                                                                                             Score 233; DB 10;
Pred. No. 9.20e-26;
26; Mismatches 79
                                                                                                                                                                                                                                                                                        2 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
1; 203B82DD
                                                                                                                                                                                                                                                                            INFR-CYS 1.
INFR-CYS 2.
50D0B435 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POXVIRIDAE; CHORDOPOXVIRINAE;
 UPDATE
                                    454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC32;
                                    À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 435
                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 11;
                                                                                                                                                                                                                              Indels
                                                                                                          168
                                                                                                                                                                                                                              10;
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RA ROTHE J. BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;

RL MOL. IMMUNOL. 30:165-175(1993).

C. -! FUNCTION: RECEPTOR FOR TWE-ALPHA.

C. -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -! SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL: M60468: G199826: -.

EMBL: M59377; G202097; -.

DR EMBL: M59377; G202097; -.

DR EMBL: M59378; G302102; -.

EMBL: M76556; G202102; -.

EMBL: M76656; G202102; JOINED.

REMBL: M76655; G202102; JOINED.
TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                    PROSITE: PS00652; TNER_NGFR.
PROSITE: PS0017; DEATH_DOMAIN.
RECEPTOR; TRANSMEMBRANE; GLYCOP
SIGNAL
1 21
PC
CHAIN
2 454
TU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 91246168.
GOODWIN R.G., ANDERSON D., JERZY R., DAV
COPELAND N.G., JENKINS N.A., SMITH C.A.;
MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 94245392.
BEBO B.F. LINTHICUM D.S.;
IMMUNOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92039815.
ROTHE J.G., BROCKHAUS M., GENTZ R., IMMUNOGENETICS 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., GRAY P.W., FELDMANN M., FOXWELL B.M.J.; EUR. J. IMMUNOL. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 91187885.

LEWIS M., TARTACLIA L.A., LEE A., BENNETT G.L., R

WONG G.H., CHEN E.Y., GOEDDEL D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 93156721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 91285014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55
TNFR1 OR THER-1,
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
   LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                          GLYCOPROTEIN; REPEAT; SIGNAL.
DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                       4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LESSLAUER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVIS T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KISSONERGHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRANNAN C.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RICE
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                            TIRL_RAT
TIRL_RAT
TIRL_RAT
P22934;
01-AUG-1991 (REL. 19, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-MOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION (P60) (THE-R1) (P55).
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                   DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                        RECEPTOR;
SIGNAL
                                                                                                                                               HSSP; P19438; LINN.
PROSITE; PS500152; TNFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
PROSITE; PS50017; DEATH_DOMAIN.
                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE; 91090841.

HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER |
LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;

DNA CELL BIOL. 9:705-715(1990).

-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; M63122; G207362; -.

B18:555; B36555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                         EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                                                                                                                                  168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>μ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                         -chagfflresecvpcshckkneec 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  msqveispcqadkdtvcgckenqfqrylsethfqcvdcspcfng-tvtipcketqntvcn 167
                                                                                                                                                                                                                                                                                                                                                                                                              RCPDGFFSNETSSKA-P-CRKHINC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yvhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasqnylrqclscktcrke 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQYVK-QECNRTHNRVCECKEG----RYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
A
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125
143
158
158
179
191
191
195
202
394
50129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%;
GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
DEATH DOMAIN.
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
21; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILAR
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 221; DB 9;
Pred. No. 2.72e-23;
                                                      TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
R -> G (IN I
486EEC09
                                                                       CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                         POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                           E M., SCHEURICH P., PFIZENMAIER K., STRATOWA C., ADOLF G.R.;
                                                                                                                                               REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REF. 6
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>6</u>).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT RE
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Best Local S
Matches 4
                                                                                                                                                                                   PIR; A60:
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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DISULFID
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CARBOHYD
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
 TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-416 FROM N.A.

MEDLINE; 90152140.

HEUER J.G., FATEMIE-NAINIE S., WHEELER E.I

DEV. BIOL. 137:287-304(1990).

-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGFR_CHICK P18519;
                                                                                                                                                                                                                                                    BOND FORMATION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARGE T.H., WESKAMP G., HELDER SHOOTER E.M., REICHARDT L.F.; NEURON 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR P
                                                                                                                                                                                                                                                                                                                                NT-3, AND NT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 90166579
LARGE T.H., WESKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOF
                                                                                                                               SIGNAL
                                                                                             DOMAIN
                                                                                                                                                                     RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GP80-LNGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                     JN0006; JN0006.
A60504; A60504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-QYVKQECNRTHNRVCECK--E-GRYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE
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| | | | | | | | :: : |:|: : |
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49; Conser
                                                                                                                                                        PS00652; TNER_NGER.
PS50017; DEATH_DOMAIN.
NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
127
146
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185
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185
201
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llarity 33.8%;
Conservative
   240
240
262
233
588
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158
158
166
179
191
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201
50969
                                                                                                                                               SIGNAL.
 19
416
239
261
416
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181
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POTENTIAL.

NGF RECEPTOR.

EXTRACELULIAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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Pred. No. 4.35e-23;
22; Mismatches 63
                                                                                                                                                                                                                                                                                                                                  FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       WHEELER E.F.,
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RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                  HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RADEKE M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
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                                                                                                                                                                                                                                                                                                                                                                      CAN
                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          BOTHWELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                      BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 461
                                                                                                                                                                                                                                                                                                                                THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISKO T.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                      TO NGF, BDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVES; NEOGNATHAE;
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                                                                                                                                                                                                                                                                                                                                DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILNE; 87051725.

JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORG
BOTHWELL M., CHAO M.;

CELL 47:545-554(1986).
-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BINI
NT-3, AND NT-4.
-!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THI
BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
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REPEAT
DOMAIN
DOMAIN
DOMAIN
DISULFID
DISU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGFR_HUMAN STANDARD; PRT; 427 AA.
P08138;
01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NUG-1995 (REL. 32, LAST ANNOTATION UPDATE)
10W-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH R
EMBL; M14764; G189205; -
PIR; A25218; GQHUN.
HSSP; P19438; ITNR.
MIM; 162010; -
PROSITE; PS00652; TNFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; PHOSPHORYLATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GP80-LNGFR).
                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sddavcrcaygyfqdelsgsckecsicevgfglmfpcrdsqdtvceecpegtfsdeanfv 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 7.1%;
Similarity 30.4%;
45; Conservative
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                                                                                                                                                                                                  A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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DEATH DOMAIN.
BY SIMILARITY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 6; L
Pred. No. 4.53e-22;
27; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA; TETRAPODA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEHGAL A., MORGAN
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REF. 2
REF. 2
CRC32;
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                                                                                                                                                                                                                                                                                                 THROUGH DISULFIDE
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Matches
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                                                                                                                                                                                                     01-APR-1988 (REL. 07
01-APR-1988 (REL. 07
01-NOV-1995 (REL. 32
LOW-AFFINITY NERVE G
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                          NGFR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
                                                      MEDLINE: 93077038.
METSIS M., TIMMUSK T., ALLIKMETS R.,
GENE 121:247-254(1992).
                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 87115859.
RADEKE M.J., MISKO T.P.,
NATURE 325:593-597(1987).
                                                                                                                                                                 RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
                                                                                                                                                        EUTHERIA; RODENTIA.
                                                                                                                                                                                             (GP80-LNGFR).
                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                              102
                                                                                          EQUENCE OF 1-22 FROM N.A.
                                                                                   ISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                          44 ckacnlgegvagpcgan-qtvcepcldsvtfsdvvsatepckpcte-cvglqsmsapcve 101
                                                                                                                                                                                                                                                                                                                                                                                                   7.0%;
Local Similarity 34.9%;
tes 45; Conservative
FUNCTION: LOW AFFINITY RECEPTOR NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A BOND FORMATION.
SUBCELLULAR LOCATION: TYPE I MEMORY.
PTM: N- AND O-GLYCOSYLATED AND I
                                                                                                                                                                                                                                                                                                       dpclpctvc 170
                                                                                                                                                                                                                                                                                                                            THNRVCECKEGRYL-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSK 157
                                                                                                                                                                                                                                                                                                                                      APCRKHTNC 166
                                                                                                                                                                                                                                                                                                                                                               CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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44
47
67
89
109
125
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                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                              07,
32,
                                                                                                                                                                         (RAT).
                                                                                                                                                                                                     07, CREATED)
07, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
GROWTH FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        60
45183
                                                                                                                     HSU
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;
                           CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
19; N
                                                                                                                                                                                                                                                                                                                                                                                                             Score 213; DB 6;
Pred. No. 1.15e-21;
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BY SIMILARITY
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4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGF RECEPTOR. EXTRACELLULAR
                                                                                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                     PRT;
I MEMBRANE PROTEIN.
AND IS PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                        EE2924BD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                     HERZENBERG
                                              WHICH CAN
                                                              SAARMA M.,
                                                                                                                                                                                                                                                    425
                                                                                                                                                                                                                                                    8
                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                     L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                              BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 427
                                                                PERSSON
                                                                                                                     SHOOTER E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                      (NGF RECEPTOR)
  o
Z
                                                                                                                                                                   MAMMALIA.
                                              NGF,
  SERINE
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Best Loc
Matches
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DISULFID
DISULFID
DISULFID
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DOMAIN
DOMAIN
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID DISULFID DISULFID
SEQUENCE FROM N.A.

MEDLINE; 96226401.

YOO J., STONE R.T., BEATTIE C.W.;

TONA CELL BIOL. 15:227-234 (1996).

-i- FUNCTION: RECEPTOR FOR A CYTO

CELL DEATH. FAS-MEDIATED APOP
                                                                              APT1 OR FAS.

BOS TAURUS (BOVINE).

EUKARYOTA; METAZOA;
                                                                                                           01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
(APO-1 ANTIGEN) (CD95).
                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00652; TNFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; X05137; E56756; -.
EMBL; X61269; -: NOT_ANNOTATED_CDS.
PIR; A26431; A26431.
HSSP; P19438; 1TNR.
                                                                                                                                                    P51867;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                             EUTHERIA; ARTIODACTYLA [1]
                                                                                                                                                                         FASA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOSPHORYLATION;
                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                        100
                                                                                                                                                                                                                                                                            103
                                                                                                                                                                                                                                   163 dpclpctvc 171
                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                           45 ckacn1gegvaqpcgan-qtvcepcldnvtfsdvvsatepckpcte-c1g1qsmsapcve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGNAL
                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                     APCRKHTNC
                                                                                                                                                                                                                                                        THNRVCECKEGRYLEIE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSK
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                                                                                                                                                                                                                                                                                                                                        Similarity
43; Conser
                                                                                                                                                                                                                                                                                                                                                                                425 AA;
                                                                                                                                                                                                                                                                                                                                      6.8%;
larity 33.3%;
Conservative
                                                                                                                                                                                                                166
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
65
100
108
123
                                                                                CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                               45432
                                                                                                                                                                                                                                                                                                                                                                                WW.
                                                                                                                                                                                                                                                                                                                                      Score 207;
Pred. No. 1.
21; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOKINE LIGAND KNOWN AS E APOPTOSIS MAY HAVE A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEATH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC
                                                                               VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                7D78F258 CRC32;
                                                                                                                                                                                                                                                                                                                                      e 207; DB 6; L. No. 1.87e-20; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR
                                                                                                                                                                         323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                       SURFACE ANTIGEN FAS
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 E IN THE
                                                                                MAMMALIA;
                                                                                                                                                                                                                                                                                                                                        5
           MEDIATES
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                              В
                                                                                                                                                                                                                                                             Ouery Match 6.2%; Score 188; DB 3; Length 323; st Local Similarity 35.7%; Pred. No. 1.08e-16; atches 40; Conservative 17; Mismatches 49; Indels 6; Gaps
                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL. U34794; G1262193; -.
                                                                                 112 vegnctrtrntkcrcksnffcnsspcehcnpcttcehgiiekctptsntkck 163
                                                                                                                                                                                                                                                                                                                                                                                                                                         POPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
                                                                 93 VKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPP-GFGVVQAGTPERNTVCK 143
                                                                                                                              37 HQLLCDKCPPGTYLKQHCTAKWKTV-CAPCPD-HYYTDSWHTSDECLYCSPVCKELQ-Y- 92
                                                                                                                                                 36445 MW;
                                                                                                                                                                                                                                                      POTENTIAL.

FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS.
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